

## SEQUENCE LISTING

<110> BASF Aktiengesellschaft

<120> D6 acetylenase and D6 desaturase from Ceratodon purpureus

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<140> US 09/980,468

<141> 2002-12-03

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<151> 1999-06-07

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<170> PatentIn Vers. 2.0

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Gly Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg  
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His Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys Lys Lys  
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Ile	His	His	Thr	Ala	Pro	Asn	Glu	Cys	Asp	Glu	Gln	Tyr	Thr	Pro	Leu
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Asp	Glu	Asp	Ile	Asp	Thr	Leu	Pro	Ile	Ile	Ala	Trp	Ser	Lys	Glu	Ile
			20					25					30		
Leu	Ala	Thr	Val	Glu	Ser	Lys	Arg	Ile	Leu	Arg	Val	Leu	Gln	Tyr	Gln
		35					40					45			
His	Tyr	Met	Ile	Leu	Pro	Leu	Leu	Phe	Met	Ala	Arg	Tyr	Ser	Trp	Thr
	50					55					60				
Phe	Gly	Ser	Leu	Leu	Phe	Thr	Phe	Asn	Pro	Asp	Leu	Ser	Thr	Thr	Lys
65					70					75					80
Gly	Leu	Ile	Glu	Lys	Gly	Thr	Val	Ala	Phe	His	Tyr	Ala	Trp	Phe	Ser
				85					90					95	
Trp	Ala	Ala	Phe	His	Ile	Leu	Pro	Gly	Val	Ala	Lys	Pro	Leu	Ala	Trp
			100					105					110		
Met	Val	Ala	Thr	Glu	Leu	Val	Ala	Gly	Leu	Leu	Leu	Gly	Phe	Val	Phe
		115					120					125			
Thr	Leu	Ser	His	Asn	Gly	Lys	Glu	Val	Tyr	Asn	Glu	Ser	Lys	Asp	Phe
	130					135					140				
Val	Arg	Ala	Gln	Val	Ile	Thr	Thr	Arg	Asn	Thr	Lys	Arg	Gly	Trp	Phe
145					150					155					160
Asn	Asp	Trp	Phe	Thr	Gly	Gly	Leu	Asp	Thr	Gln	Ile	Glu			
				165					170						

<210> 7  
 <211> 514  
 <212> DNA  
 <213> Ceratodon purpureus

<400> 7

cctgcatcat gctgctccga atgaatgcga ccaaaagtac acgccgattg atgaggatat 60  
 tgatactctc cccatcattg cttggagtaa agatctcttg gccactgttg agagcaagac 120  
 catgttgcca gttcttcagt accagcacct attctttttg gttcttttga cgtttgcccg 180

ggcgagttgg ctatTTTtTgga ggcgcggcctt cactctcagg cccgagttga cccttggcga 240  
 gaagctTTtTg gagaggggaa cgatggcTTt gcactacatt tggTTtTaata gtgttgcgTt 300  
 ttatctgctc cccggatgga aaccagtTgt atggatggTg gtcagcgagc tcatgtctgg 360  
 tttcctgctg ggatacgtat ttgtactcag tcacaatgga atggaggtgt acaatacgtc 420  
 aaaggacttc gtgaatgccc agattgcacT gactcgcgac atcaaagcag gggTgtTTaa 480  
 tgattggTtc accggaggtc tcaacagaca gatt 514

<210> 8

<211> 172

<212> PRT

<213> Ceratodon purpureus

<400> 8

Leu	His	His	Ala	Ala	Pro	Asn	Glu	Cys	Asp	Gln	Lys	Tyr	Thr	Pro	Ile
1				5					10					15	
Asp	Glu	Asp	Ile	Asp	Thr	Leu	Pro	Ile	Ile	Ala	Trp	Ser	Lys	Asp	Leu
			20					25					30		
Leu	Ala	Thr	Val	Glu	Ser	Lys	Thr	Met	Leu	Arg	Val	Leu	Gln	Tyr	Gln
			35				40					45			
His	Leu	Phe	Phe	Leu	Val	Leu	Leu	Thr	Phe	Ala	Arg	Ala	Ser	Trp	Leu
	50					55				60					
Phe	Trp	Ser	Ala	Ala	Phe	Thr	Leu	Arg	Pro	Glu	Leu	Thr	Leu	Gly	Glu
65					70					75					80
Lys	Leu	Leu	Glu	Arg	Gly	Thr	Met	Ala	Leu	His	Tyr	Ile	Trp	Phe	Asn
				85					90					95	
Ser	Val	Ala	Phe	Tyr	Leu	Leu	Pro	Gly	Trp	Lys	Pro	Val	Val	Trp	Met
			100					105					110		
Val	Val	Ser	Glu	Leu	Met	Ser	Gly	Phe	Leu	Leu	Gly	Tyr	Val	Phe	Val
		115					120					125			
Leu	Ser	His	Asn	Gly	Met	Glu	Val	Tyr	Asn	Thr	Ser	Lys	Asp	Phe	Val
	130					135					140				
Asn	Ala	Gln	Ile	Ala	Ser	Thr	Arg	Asp	Ile	Lys	Ala	Gly	Val	Phe	Asn
145					150					155					160
Asp	Trp	Phe	Thr	Gly	Gly	Leu	Asn	Arg	Gln	Ile	Glu				
				165					170						

<210> 9

<211> 535

<212> DNA

<213> Ceratodon purpureus

&lt;400&gt; 9

tgctcatcac atcgcttgta atagtataga atatgatcca gacctacagt acatccccct 60  
 ttttgcagtg acatcaaagc tcttctctaa cctctactcc tacttctatg aaagggttat 120  
 gccattcgat ggcgtagcac gctctctgat tgcctaccag cactggacgt tttatccaat 180  
 aatggctggt gctcgggtga acctctttgc ccaatccctt ctagtactga cctcgaagaa 240  
 gcatgtgcc aacaggtggc ttgagctcgg tgctatcggg ttcttctacc tgtgggttctt 300  
 caccctcttg tcgtacctgc ccactgcacc ggagaggett gctttcgtcc ttgtcagttt 360  
 tgcagtgaca gggatccagc atgtacagtt ttgcctgaac cacttctcat cgccgggttta 420  
 tctaggacag ccgaagagca aggcttgggt tgaatctcaa gcacggggca ctctcaatct 480  
 ctctacaccg gcttacatgg attggtttca cggggggtctt cagttccaga tcgag 535

&lt;210&gt; 10

&lt;211&gt; 178

&lt;212&gt; PRT

<213> *Ceratodon purpureus*

&lt;400&gt; 10

Ala	His	His	Ile	Ala	Cys	Asn	Ser	Ile	Glu	Tyr	Asp	Pro	Asp	Leu	Gln	1	5	10	15
Tyr	Ile	Pro	Leu	Phe	Ala	Val	Thr	Ser	Lys	Leu	Phe	Ser	Asn	Leu	Tyr	20	25	30	
Ser	Tyr	Phe	Tyr	Glu	Arg	Val	Met	Pro	Phe	Asp	Gly	Val	Ala	Arg	Ser	35	40	45	
Leu	Ile	Ala	Tyr	Gln	His	Trp	Thr	Phe	Tyr	Pro	Ile	Met	Ala	Val	Ala	50	55	60	
Arg	Val	Asn	Leu	Phe	Ala	Gln	Ser	Leu	Leu	Val	Leu	Thr	Ser	Lys	Lys	65	70	75	80
His	Val	Pro	Asp	Arg	Trp	Leu	Glu	Leu	Gly	Ala	Ile	Gly	Phe	Phe	Tyr	85	90	95	
Leu	Trp	Phe	Phe	Thr	Leu	Leu	Ser	Tyr	Leu	Pro	Thr	Ala	Pro	Glu	Arg	100	105	110	
Leu	Ala	Phe	Val	Leu	Val	Ser	Phe	Ala	Val	Thr	Gly	Ile	Gln	His	Val	115	120	125	
Gln	Phe	Cys	Leu	Asn	His	Phe	Ser	Ser	Pro	Val	Tyr	Leu	Gly	Gln	Pro	130	135	140	
Lys	Ser	Lys	Ala	Trp	Val	Glu	Ser	Gln	Ala	Arg	Gly	Thr	Leu	Asn	Leu	145	150	155	160
Ser	Thr	Pro	Ala	Tyr	Met	Asp	Trp	Phe	His	Gly	Gly	Leu	Gln	Phe	Gln				

165

170

175

Ile Glu

&lt;210&gt; 11

&lt;211&gt; 2160

&lt;212&gt; DNA

&lt;213&gt; Ceratodon purpureus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (159) .. (1721)

&lt;400&gt; 11

cggaggtctc ttgtcgttct tggagtcctgt gtcgagcttg gaatgcggta ggcgcggccg 60

tttcgtgggt ttggcgttgg cattgcgcga gggcggacag tgggagtgcg ggaggtctgt 120

ttgtgcatga cgaggtgggt gtaatcttcg ccggcaga atg gtg tcc cag ggc ggc 176  
 Met Val Ser Gln Gly Gly  
 1 5

ggt ctc tcg cag ggt tcc att gaa gaa aac att gac gtt gag cac ttg 224  
 Gly Leu Ser Gln Gly Ser Ile Glu Glu Asn Ile Asp Val Glu His Leu  
 10 15 20

gca acg atg ccc ctc gtc agt gac ttc cta aat gtc ctg gga acg act 272  
 Ala Thr Met Pro Leu Val Ser Asp Phe Leu Asn Val Leu Gly Thr Thr  
 25 30 35

ttg ggc cag tgg agt ctt tcc act aca ttc gct ttc aag agg ctc acg 320  
 Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe Ala Phe Lys Arg Leu Thr  
 40 45 50

act aag aaa cac agt tcg gac atc tcg gtg gag gca caa aaa gaa tcg 368  
 Thr Lys Lys His Ser Ser Asp Ile Ser Val Glu Ala Gln Lys Glu Ser  
 55 60 65 70

gtt gcg cgg ggg cca gtt gag aat att tct caa tcg gtt gcg cag ccc 416  
 Val Ala Arg Gly Pro Val Glu Asn Ile Ser Gln Ser Val Ala Gln Pro  
 75 80 85

atc agg cgg agg tgg gtg cag gat aaa aag ccg gtt act tac agc ctg 464  
 Ile Arg Arg Arg Trp Val Gln Asp Lys Lys Pro Val Thr Tyr Ser Leu  
 90 95 100

aag gat gta gct tcg cac gat atg ccc cag gac tgc tgg att ata atc 512  
 Lys Asp Val Ala Ser His Asp Met Pro Gln Asp Cys Trp Ile Ile Ile  
 105 110 115

aaa gag aag gtg tat gat gtg agc acc ttc gct gag cag cac cct gga 560  
 Lys Glu Lys Val Tyr Asp Val Ser Thr Phe Ala Glu Gln His Pro Gly  
 120 125 130

ggc acg gtt atc aac acc tac ttc gga cga gac gcc aca gat gtt ttc 608  
 Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg Asp Ala Thr Asp Val Phe  
 135 140 145 150

tct	act	ttc	cac	gca	tcc	acc	tca	tgg	aag	att	ctt	cag	aat	ttc	tac	656
Ser	Thr	Phe	His	Ala	Ser	Thr	Ser	Trp	Lys	Ile	Leu	Gln	Asn	Phe	Tyr	
				155					160					165		
atc	ggg	aac	ctt	ggt	agg	gag	gag	ccg	act	ttg	gag	ctg	ctg	aag	gag	704
Ile	Gly	Asn	Leu	Val	Arg	Glu	Glu	Pro	Thr	Leu	Glu	Leu	Leu	Lys	Glu	
			170					175					180			
tac	aga	gag	ttg	aga	gcc	ctt	ttc	ttg	aga	gaa	cag	ctt	ttc	aag	agt	752
Tyr	Arg	Glu	Leu	Arg	Ala	Leu	Phe	Leu	Arg	Glu	Gln	Leu	Phe	Lys	Ser	
		185					190					195				
tcc	aaa	tcc	tac	tac	ctt	ttc	aag	act	ctc	ata	aat	gtt	tcc	att	gtt	800
Ser	Lys	Ser	Tyr	Tyr	Leu	Phe	Lys	Thr	Leu	Ile	Asn	Val	Ser	Ile	Val	
	200					205					210					
gcc	aca	agc	att	gcg	ata	atc	agt	ctg	tac	aag	tct	tac	cgg	gcg	gtt	848
Ala	Thr	Ser	Ile	Ala	Ile	Ile	Ser	Leu	Tyr	Lys	Ser	Tyr	Arg	Ala	Val	
215					220					225					230	
ctg	tta	tca	gcc	agt	ttg	atg	ggc	ttg	ttt	att	caa	cag	tgc	gga	tgg	896
Leu	Leu	Ser	Ala	Ser	Leu	Met	Gly	Leu	Phe	Ile	Gln	Gln	Cys	Gly	Trp	
				235					240					245		
ttg	tct	cac	gat	ttt	cta	cac	cat	cag	gta	ttt	gag	aca	cgc	tgg	ctc	944
Leu	Ser	His	Asp	Phe	Leu	His	His	Gln	Val	Phe	Glu	Thr	Arg	Trp	Leu	
			250					255					260			
aat	gac	gtt	gtt	ggc	tat	gtg	gtc	ggc	aac	gtt	gtt	ctg	gga	ttc	agt	992
Asn	Asp	Val	Val	Gly	Tyr	Val	Val	Gly	Asn	Val	Val	Leu	Gly	Phe	Ser	
		265					270					275				
gtc	tcg	tgg	tgg	aag	acc	aag	cac	aac	ctg	cat	cat	gct	gct	ccg	aat	1040
Val	Ser	Trp	Trp	Lys	Thr	Lys	His	Asn	Leu	His	His	Ala	Ala	Pro	Asn	
	280					285					290					
gaa	tgc	gac	caa	aag	tac	aca	ccg	att	gat	gag	gat	att	gat	act	ctc	1088
Glu	Cys	Asp	Gln	Lys	Tyr	Thr	Pro	Ile	Asp	Glu	Asp	Ile	Asp	Thr	Leu	
295					300				305						310	
ccc	atc	att	gct	tgg	agt	aaa	gat	ctc	ttg	gcc	act	gtt	gag	agc	aag	1136
Pro	Ile	Ile	Ala	Trp	Ser	Lys	Asp	Leu	Leu	Ala	Thr	Val	Glu	Ser	Lys	
				315					320					325		
acc	atg	ttg	cga	gtt	ctt	cag	tac	cag	cac	cta	ttc	ttt	ttg	gtt	ctt	1184
Thr	Met	Leu	Arg	Val	Leu	Gln	Tyr	Gln	His	Leu	Phe	Phe	Leu	Val	Leu	
			330					335					340			
ttg	acg	ttt	gcc	cgg	gcg	agt	tgg	cta	ttt	tgg	agc	gcg	gcc	ttc	act	1232
Leu	Thr	Phe	Ala	Arg	Ala	Ser	Trp	Leu	Phe	Trp	Ser	Ala	Ala	Phe	Thr	
		345					350					355				
ctc	agg	ccc	gag	ttg	acc	ctt	ggc	gag	aag	ctt	ttg	gag	agg	gga	acg	1280
Leu	Arg	Pro	Glu	Leu	Thr	Leu	Gly	Glu	Lys	Leu	Leu	Glu	Arg	Gly	Thr	
	360					365					370					
atg	gct	ttg	cac	tac	att	tgg	ttt	aat	agt	gtt	gcg	ttt	tat	ctg	ctc	1328
Met	Ala	Leu	His	Tyr	Ile	Trp	Phe	Asn	Ser	Val	Ala	Phe	Tyr	Leu	Leu	

375	380	385	390	
ccc gga tgg aaa cca gtt gta tgg atg gtg gtc agc gag ctc atg tct				1376
Pro Gly Trp Lys Pro Val Val Trp Met Val Val Ser Glu Leu Met Ser				
	395	400	405	
ggt ttc ctg ctg gga tac gta ttt gta ctc agt cac aat gga atg gag				1424
Gly Phe Leu Leu Gly Tyr Val Phe Val Leu Ser His Asn Gly Met Glu				
	410	415	420	
gtg tac aat acg tca aag gac ttc gtg aat gcc cag att gca tcg act				1472
Val Tyr Asn Thr Ser Lys Asp Phe Val Asn Ala Gln Ile Ala Ser Thr				
	425	430	435	
cgc gac atc aaa gca ggg gtg ttt aat gat tgg ttc acc gga ggt ctc				1520
Arg Asp Ile Lys Ala Gly Val Phe Asn Asp Trp Phe Thr Gly Gly Leu				
	440	445	450	
aac aga .cag att gag cat cat cta ttt cca acg atg ccc agg cac aac				1568
Asn Arg Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn				
	455	460	465	470
ctt aat aaa att tct cct cac gtg gag act ttg tgc aag aag cat gga				1616
Leu Asn Lys Ile Ser Pro His Val Glu Thr Leu Cys Lys Lys His Gly				
	475	480	485	
ctg gtc tac gaa gac gtg agc atg gct tcg ggc act tac cgg gtt ttg				1664
Leu Val Tyr Glu Asp Val Ser Met Ala Ser Gly Thr Tyr Arg Val Leu				
	490	495	500	
aaa aca ctt aag gac gtt gcc gat gct gct tca cac cag cag ctt gct				1712
Lys Thr Leu Lys Asp Val Ala Asp Ala Ala Ser His Gln Gln Leu Ala				
	505	510	515	
gcg agt tga ggcacgcag cactcgtcga aacatttttg tctgttatag				1761
Ala Ser				
	520			
tggtcatatg tgatcgaggg gaaaagggtcc catgctctga tctattcttc tgtagccaat				1821
atttttcaat tgaaaggagg ttcttcactt atcttccatc tatcgttgca catcctgcat				1881
cagagttagc gttggagtaa tgtaagcac ttgtagatta tgcccacat tgccacattt				1941
ctgttcggtt acaatcgttt gattccatgc tatcctccgt gttcatctcg ttgttataag				2001
caagcttgaa aaaacatgct acgagattgg cagacgttgt cttggcagct gtagaggttg				2061
gttccattca ttgtgtagta cagaactctc tcgtccctgt ttctctacat tacttgttac				2121
atagtgactt tcattcacag caaaaaaaaaa aaaaaaaaaa				2160

&lt;210&gt; 12

&lt;211&gt; 520

&lt;212&gt; PRT

&lt;213&gt; Ceratodon purpureus

&lt;400&gt; 12

Met Val Ser Gln Gly Gly Gly Leu Ser Gln Gly Ser Ile Glu Glu Asn  
 1 5 10 15  
 Ile Asp Val Glu His Leu Ala Thr Met Pro Leu Val Ser Asp Phe Leu  
 20 25 30  
 Asn Val Leu Gly Thr Thr Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe  
 35 40 45  
 Ala Phe Lys Arg Leu Thr Thr Lys Lys His Ser Ser Asp Ile Ser Val  
 50 55 60  
 Glu Ala Gln Lys Glu Ser Val Ala Arg Gly Pro Val Glu Asn Ile Ser  
 65 70 75 80  
 Gln Ser Val Ala Gln Pro Ile Arg Arg Arg Trp Val Gln Asp Lys Lys  
 85 90 95  
 Pro Val Thr Tyr Ser Leu Lys Asp Val Ala Ser His Asp Met Pro Gln  
 100 105 110  
 Asp Cys Trp Ile Ile Ile Lys Glu Lys Val Tyr Asp Val Ser Thr Phe  
 115 120 125  
 Ala Glu Gln His Pro Gly Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg  
 130 135 140  
 Asp Ala Thr Asp Val Phe Ser Thr Phe His Ala Ser Thr Ser Trp Lys  
 145 150 155 160  
 Ile Leu Gln Asn Phe Tyr Ile Gly Asn Leu Val Arg Glu Glu Pro Thr  
 165 170 175  
 Leu Glu Leu Leu Lys Glu Tyr Arg Glu Leu Arg Ala Leu Phe Leu Arg  
 180 185 190  
 Glu Gln Leu Phe Lys Ser Ser Lys Ser Tyr Tyr Leu Phe Lys Thr Leu  
 195 200 205  
 Ile Asn Val Ser Ile Val Ala Thr Ser Ile Ala Ile Ile Ser Leu Tyr  
 210 215 220  
 Lys Ser Tyr Arg Ala Val Leu Leu Ser Ala Ser Leu Met Gly Leu Phe  
 225 230 235 240  
 Ile Gln Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val  
 245 250 255  
 Phe Glu Thr Arg Trp Leu Asn Asp Val Val Gly Tyr Val Val Gly Asn  
 260 265 270  
 Val Val Leu Gly Phe Ser Val Ser Trp Trp Lys Thr Lys His Asn Leu  
 275 280 285  
 His His Ala Ala Pro Asn Glu Cys Asp Gln Lys Tyr Thr Pro Ile Asp  
 290 295 300  
 Glu Asp Ile Asp Thr Leu Pro Ile Ile Ala Trp Ser Lys Asp Leu Leu



305                      310                      315                      320  
 Ala Thr Val Glu Ser Lys Thr Met Leu Arg Val Leu Gln Tyr Gln His  
                                  325                      330                      335  
 Leu Phe Phe Leu Val Leu Leu Thr Phe Ala Arg Ala Ser Trp Leu Phe  
                                  340                      345                      350  
 Trp Ser Ala Ala Phe Thr Leu Arg Pro Glu Leu Thr Leu Gly Glu Lys  
                                  355                      360                      365  
 Leu Leu Glu Arg Gly Thr Met Ala Leu His Tyr Ile Trp Phe Asn Ser  
                                  370                      375                      380  
 Val Ala Phe Tyr Leu Leu Pro Gly Trp Lys Pro Val Val Trp Met Val  
                                  385                      390                      395                      400  
 Val Ser Glu Leu Met Ser Gly Phe Leu Leu Gly Tyr Val Phe Val Leu  
                                  405                      410                      415  
 Ser His Asn Gly Met Glu Val Tyr Asn Thr Ser Lys Asp Phe Val Asn  
                                  420                      425                      430  
 Ala Gln Ile Ala Ser Thr Arg Asp Ile Lys Ala Gly Val Phe Asn Asp  
                                  435                      440                      445  
 Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro  
                                  450                      455                      460  
 Thr Met Pro Arg His Asn Leu Asn Lys Ile Ser Pro His Val Glu Thr  
                                  465                      470                      475                      480  
 Leu Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Met Ala Ser  
                                  485                      490                      495  
 Gly Thr Tyr Arg Val Leu Lys Thr Leu Lys Asp Val Ala Asp Ala Ala  
                                  500                      505                      510  
 Ser His Gln Gln Leu Ala Ala Ser  
                                  515                      520

<210> 13  
 <211> 20  
 <212> DNA  
 <213> artificial sequence

<220>  
 <221> modified\_base  
 <222> 15  
 <223> 15 is inosine

<400> 13

tggtggaart ggamncayaa

20

<210> 14  
 <211> 20

<212> DNA  
 <213> artificial sequence  
 <220>  
 <221> modified\_base  
 <222> 3, 12, 15  
 <223> 3, 12, 15 are inosine  
 <400> 14

kgntggaark rnmancayaa

20

<210> 15  
 <211> 20  
 <212> DNA  
 <213> artificial sequence  
 <220>  
 <221> 3, 6, 12  
 <222> 3, 6, 12 are any nucleotide  
 <223> sequencing primer  
 <400> 15

atntknggra anarrtgrtg

20

<210> 16  
 <211> 18  
 <212> DNA  
 <213> artificial sequence  
 <220>  
 <223> sequencing primer  
 <400> 16

cgaatgagtg cgacgaac

18

<210> 17  
 <211> 18  
 <212> DNA  
 <213> artificial sequence  
 <220>  
 <223> sequencing primer  
 <400> 17

aataacctgg gctctcac

18

<210> 18  
 <211> 20  
 <212> DNA  
 <213> artificial sequence

<220>  
<223> sequencing primer

<400> 18

atgaggatat tgatactctc

20

<210> 19  
<211> 18  
<212> DNA  
<213> artificial sequence

<220>  
<223> sequencing primer

<400> 19

gcaatctggg cattcacg

18

<210> 20  
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<212> DNA  
<213> artificial sequence

<220>  
<223> sequencing primer

<400> 20

gacatcaaag ctcttctc

18

<210> 21  
<211> 18  
<212> DNA  
<213> artificial sequence

<220>  
<223> sequencing primer

<400> 21

ggcgatgag aagtggttc

18

<210> 22  
<211> 26  
<212> DNA  
<213> artificial sequence

<220>  
<223> sequencing primer

<400> 22

ccggtaccat ggccctcggt accgac

26

<210> 23  
 <211> 26  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> sequencing primer

<400> 23

ccgaattctt agtgagcgtg aagccg

26

<210> 24  
 <211> 26  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> sequencing primer

<400> 24

ccggtaccat ggtgtcccag ggcggc

26

<210> 25  
 <211> 26  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> sequencing primer

<400> 25

ccgaattctc aactcgcagc aagctg

26

<210> 26  
 <211> 31  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> sequencing primer

<400> 26

aaaaggatcc aaaatggccc tcgttaccga c

31

<210> 27  
 <211> 27

<212> DNA  
<213> artificial sequence

<220>  
<223> sequencing primer

<400> 27

aaaagtcgac ttagtgagcg tgaagcc

27

<210> 28  
<211> 60  
<212> DNA  
<213> artificial sequence

<220>  
<223> sequencing primer

<400> 28

gtcgaccgc ggactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa

60